Supplemental Figure 1. Melting curves of analyzed genes, *ACT* (A), *CAC* (B), *EXPRESSED* (C), *GAPDH* (D), *PP2a* (E), *RPL8* (F), *SAND* (G), *TIP41* (H), *FUL1* (I), *AP2c* (J), *SIYABBY1a* (K), and *SIYABBY2a* (L). All qRT-PCR reaction resulted in a unique single peak. Arrowheads indicate a peak from no template controls.

Supplemental Figure 2. Gel electrophoresis of qRT-PCR products with 2 % agarose gel. (A) Amplicons obtained from qRT-PCR with cDNA templates. (B) Amplicons of no template controls. Each lane indicate the followings: primer pairs target to *ACT* (1), *CAC* (2), *EXPRESSED* (3), *GAPDH* (4), *PP2a* (5), *RPL8* (6), *SAND* (7), *TIP41* (8), *FUL1* (9), *AP2c* (10), *SIYABBY1a* (11), and *SIYABBY2a* (12).

Supplemental Figure 3. Expression profile of *SIYABBY1a* normalized with two stable genes (*EXPRESSED*; A, *TIP41*; B) and two unstable genes (*ACT*; C and *RPL8*; D). The relative expression levels at "open flower pistil" (arrows) were adjusted to 1. White bars indicate the expressions in stamens. Error bars represent the standard error of the mean.

Supplemental Figure 4. Expression profiles of *FUL1* normalized with two stable genes (*EXPRESSED*; A, *TIP41*; B) and two unstable genes (*ACT*; C and *RPL8*; D). For relative representation, the expression levels at "1 cm fruit" stages (arrows) were adjusted to 1. White bars indicate the expressions in stamens. Error bars represent the standard error of the mean.

Supplemental figure 5. Expression profiles of *AP2c* normalized with two stable genes (*EXPRESSED*; A, *TIP41*; B) and two unstable genes (*ACT*; C and *RPL8*; D). For relative representation, the expression levels at "orange fruit" stages (arrows) were adjusted to 1. White bars indicate the expressions in stamens. Error bars represent the standard error of the mean.









